Please replace the paragraph beginning on page 1 lines 24-26 with the following paragraph:

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This invention relates to a method and computer program product for quantitative analysis of a nucleic acid amplification reaction.

IN THE CLAIMS

Please cancel claims 1-44 and Add new claims 45-57.

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45. A method for quantification of the concentration of a nucleic acid in a sample, comprising the steps of:
    a) mixing the sample with an amplification reagent;
    b) amplifying at least one nucleic acid sequence in the sample to create a nucleic acid amplification product;
    c) determining the amount of the nucleic acid amplification product as a function of amplification reaction time;
    d) calculating a derivative of said function;
    e) determining the maximum of said derivative; and
    f) calculating from said maximum the initial concentration of the nucleic acid sequence in the sample.

46. The method of claim 45, wherein during one phase of the amplification reaction the amount of amplification product increases progressively and wherein after said progressive phase, the rate of amplification decreases.

47. The method of claim 45, wherein the amount of the amplification product is determined during a logarithmic growth phase of the amplification reaction.

48. The method of claim 45, wherein the amplification product is detected by means of fluorescence.

49. The method of claim 46, wherein the amplification is obtained by a polymerase chain reaction and the amplification product is detected by an intercalating dye.

50. The method of claim 48, wherein amplification is obtained by a polymerase chain reaction and the amplification product is detected by two polynucleotide probes, each labeled with a fluorescent entity, such that when both probes are hybridized to one strand of the nucleic acid amplification product, fluorescence resonance energy transfer occurs between the two fluorescent entities.

51. The method of claim 47, wherein said derivative is calculated by a mathematical fit.

52. The method of claim 51 wherein the amplification product is detected by means of fluorescence.

53. The method of claim 51, wherein the amplification is obtained by a polymerase chain reaction and the amplification product is detected by an intercalating dye.

54. The method of claim 45, wherein the step of calculating the derivative of said function comprises calculating the second derivative.

55. The method of claim 45, wherein the step of calculating the derivative of said function comprises calculating, the first derivative.

56. A method for quantification of the concentration of a nucleic acid in a sample, comprising the steps of:

a) mixing the sample with an amplification reagent;

b) amplifying at least one nucleic acid sequence in the sample to create a nucleic acid amplification product;

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c) determining the amount of the nucleic acid amplification product as a function of amplification reaction time;

d) calculating the second derivative of said function;

e) determining the maximum of said second derivative; and

f) calculating from said maximum the initial concentration of the nucleic acid sequence in the sample.

57. A method for quantification of the concentration of a nucleic acid in a test sample, comprising the steps of:

a) mixing the test sample with an amplification reagent;

b) amplifying at least one nucleic acid sequence in the test sample by a process comprising the step of subjecting the test sample to a number of amplification cycles to create a nucleic acid amplification product;

c) determining a value corresponding to the relative amount of the nucleic acid amplification product for each amplification cycle to generate a data set;

d) generating a function from said data set;

e) calculating a derivative of said function;

f) determining a fractional cycle number corresponding to a maximum of said derivative;

g) obtaining a calibration curve generated using steps a-e on a plurality of additional nucleic acid calibration samples, each additional calibration sample having a known concentration of the nucleic acid sequence; and

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h) determining the initial concentration of the nucleic acid sequence in the test sample using the calibration curve.

[redacted]